Exploring Genetic Distinctiveness among Radish (*Raphanus sativus* L.) Strains

Abstract

The field experiment was carried out using the twenty genotypes of radish and evaluated during the Rabi season, 2021–2022, at the experimental unit of the Department of Horticulture, Tilak Dhari PG College, Jaunpur (U.P.). The objective was to estimate the genetic diversity available in the genotypes. The D^2 analysis showed broad diversity among the genotypes, which was grouped into five clusters on the basis of various horticultural traits. The clustering pattern showed that the highest genotypes were recorded in cluster III (8 genotypes), followed by cluster V (5 genotypes), cluster IV (3 genotypes), cluster II (2 genotypes), and cluster I (2 genotypes). The greatest intra-cluster distance was recorded in Cluster IV (3.380), followed by Cluster III (3.219), Cluster II (3.104), and Cluster V (3.079). Cluster I have the smallest intra-cluster distance (2.182). The highest inter-cluster distance was 6.851 observed between Cluster IV and II, while the lowest was 3.139 between Cluster V and III. By the divergence analysis, the parents for hybridization for diverse clusters could be selected to harness the heterotic vigour's and also to minimize the genetic erosion. The selection of the best genotype for breeding programs for the development of high-yielding varieties.

Keywords: Radish, genetic divergence, distinctiveness, clusters, D^2 statistics, disparity, strains.

Introduction

Radish (*Raphanus sativus* L., 2n = 18) is an important kitchen garden crop and cash crop. The word radish is said to have been derived from 'radix', the Latin word for root. The genus *Raphanus*, derived from the Latin word 'raphanos,' meaning 'easily reared', belongs to the family Brassicaceae. In India, radish is cultivated on an area of 204,000 ha with a total production of 3107,000 MT [1]. Radish is an erect annual or biennial herb depending on type. The leaves are varied, ranging from 10–15 cm in small-rooted cultivars to as much as 45 cm in large-rooted cultivars. The edible portion of radish roots (fusiform) develops from both the primary root and the hypocotyls. Radish roots vary greatly in shape, size, and colour. It has rosette leaves that vary in morphology. The inflorescence of radish is a typical terminal, erect, long, many-flowered raceme of Brassicaceae. The flower is bisexual. Fruits are cylindrical siliqua. Beside the roots, the green leaves and pods are commonly consumed raw or cooked as vegetables. It is a cross-pollinated vegetable due to sporophytic self-incompatibility and protogyny in nature; the mode of pollination is entomophilous. The characteristic pungent flavour and taste of radish roots is due to the high volatile isothiocyanate alkaloid content (trans-4 methyl thiobutenyl isothiocyanate), which is more synthesized at high temperatures. It is used for neurological headache, sleeplessness, and chronic diarrhoea, especially preventing it in cases of jaundice, piles, stone formation in the urinary tract, increased appetite, and problems with the liver and spleen [2]. Radish has a cooling effect and prevents constipation [3]. Radish is predominantly a cool-season crop and is divided into two groups: tropical and temperate. Tropical types can tolerate higher temperatures than temperate types. The tropical type produces roots and seeds in both tropical and temperate climates. However, the temperate type produces roots under both climatic conditions, but its seed can only be produced in a temperate climate.

The genetic improvement of the crop depends on the amount of genetic variability present in the population, and the germplasm serves as a valuable source for the base population and provides the possibility for wide variability [4]. In any crop improvement program, genetic diversity plays a very important role as it helps in selecting the suitable parents for hybridization, resulting in superior hybrids and desirable recombinants [5]. Genetic diversity can be worked out with the help of D^2 analysis, which was given by Mahalanobis (1936) [6]. Rao (1952) proposed this method for the first time to measure the genetic diversity of plants [7]. It is a very potent technique for measuring genetic divergence. Now it is reliably and extensively used in plants for measuring genetic divergence [8,9]. The aim of forming clusters and finding intra- and inter-cluster divergence is to provide the basis for selecting parents for a planned breeding program. Keeping in view the above facts, the present investigation was undertaken to work out genetic divergence among 20 genotypes based on eighteen important traits of radish to help the breeders in selecting promising and genetically diverse parents for the desired improvement.

Materials and Methods

The experiment comprising twenty diverse genotypes of radish was carried out in a randomized block design with three replications during the Rabi season of the year 2021 at the experimental unit of the Department of Horticulture, Tilak Dhari PG College, Jaunpur (U.P.). Geographically, Jaunpur is situated in the eastern part of Uttar Pradesh, which lies between 25° 44' 0" north latitude and 82° 41' 0" east longitude at an elevation of 83.230 m above mean sea level. The genotypes were randomly allotted to the plots in each replication, with row to row and plant to plant spacing of 30 cm × 10 cm. The package of practices was followed as per the recommendations for raising a good and healthy crop. Five plants were selected in each plot in each replication, excluding border plants, for recording and observation. Data were recorded on eighteen characters, namely, seed germination (%), height of plants (cm), number of leaves per plant, length of leaves (cm), width of leaves (cm), days taken to maturity, average plant weight (gm), average root weight (gm), crown diameter (mm), length of root (cm), diameter of root (mm), root yield per plot (Kg), root yield per ha (Q), root/shoot ratio (on a weight and length basis), total soluble solids (°Brix), ascorbic acid (mg/100g), dry matter (%).

Genetic divergence between groups was estimated using D^2 statistics given by Mahalanobis (1936) [6]. All eighteen traits were correlated and transformed into uncorrelated linear combinations through the computer. The mean values of the uncorrelated linear combination were computed to calculate D^2 values between all possible pairs of genotypes. Rao (1952) described how Tocher's approach was used to grouping of genotypes [7]. The criterion used in clustering by this method is that varieties belonging to the same cluster should show a smaller D^2 value than those belonging to different clusters.

Plate: Field view & uprooted radish

Result and Discussion

Group constellation: On the basis of D^2 statistics, five clusters were formed from twenty genotypes of radish. The composition of clusters is given in Table 1. The maximum number of genotypes (8) were accommodated in clusters III and V (5), followed by cluster IV (3), cluster II (2) and cluster I (2). The genotypes included in cluster I were Ivory White and Kalyani White, whereas in cluster II they were Japanese White and Pusa Chetki. The cluster III had eight genotypes (All Season, CO.1, Kalyanpur No.-1, Kashi Aardra, Kashi Mooli 40, Kashi Sweta, Mino Early, and Pusa Reshmi). Cluster IV was comprised of three genotypes (Kashi Hans, Punjab Ageti, and Punjab Safed). while the remaining five genotypes (Hisar Mooli No. 1, Punjab Pasand, Pusa Desi, Pusa Himani, and White Icicle) were placed in a V cluster. The cluster analysis using Tocher's method grouped 20 radish genotypes into five non-overlapping clusters for the discrimination of varietal lines into discrete clusters and indicated the presence of a substantial amount of diversity in the material evaluated. This was in conformism with the findings of some earlier workers [10,11]. The presence of substantial genetic divergence among the genotypes screened in the present investigation suggested that this material might serve as a good source for selecting the diverse parents for a hybridization program aimed at isolating desirable combinations for root yield as well as other characters.

Table 1: Distribution of 20 genotypes of radish to different clusters on the basis of D^2 statistics

Clusters	**No of genotypes**	**Genotypes**
I	2	Ivory White, Kalyani White
II	2	Japanese White, Pusa Chetki
III	8	All Season, CO.1, Kalyanpur No.-1, Kashi Aardra, Kashi Mooli 40, Kashi Sweta, Mino Early, Pusa Reshmi
IV	3	Kashi Hans, Punjab Ageti, Punjab Safed
V	5	Hisar Mooli No. 1, Punjab Pasand, Pusa Desi, Pusa

		Himani, White Icicle

Inter-cluster and Intra-cluster Distances: The perusal of intra-cluster and inter-cluster distances (Table 2) revealed that inter-cluster values were greater than intra-cluster distance values. The intra-cluster D^2 values ranged from 2.182 (cluster I) to 3.380 (cluster IV). The intra-cluster distance was maximum 3.380 in cluster IV and 3.219 in cluster III, followed by 3.104 in cluster II, 3.079 in cluster V, and 2.182 in cluster I. While the inter-cluster distance was maximum 6.851 between cluster IV and II, it was followed by 5.437 between cluster II and I, 5.281 between cluster IV and I, 5.041 between cluster V and I, 5.030 between cluster V and IV, 5.023 between cluster V and II, 5.017 between cluster III and II, 4.730 between cluster IV and III, 3.403 between cluster III and I, and 3.139 between cluster V and III. The selection of parents from highly diverse genotypes for hybridization work gives a range of useful combinations that result in highly heterotic hybrids. Many earlier workers indicated the significance of genetic divergence [12,13,14,15].

Table 2: Average intra-cluster and inter-cluster value for 20 genotypes of radish

Clusters	**I**	**II**	**III**	**IV**	**V**
I	**2.182**				
II	5.437	**3.104**			
III	3.403	5.017	**3.219**		
IV	5.281	6.851	4.730	**3.380**	
V	5.041	5.023	3.139	5.030	**3.079**

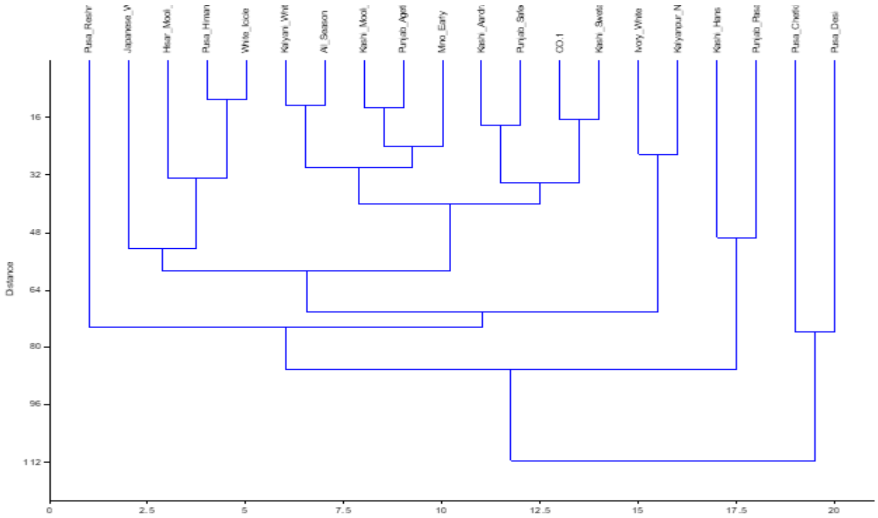

Fig 1: Dendrogram showing the intra and inter-cluster D^2 values

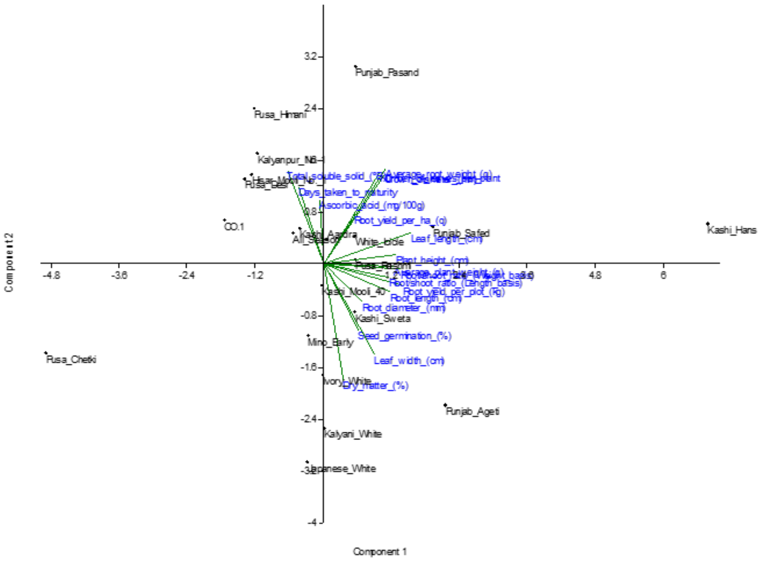

Fig 2: Clustering pattern of different group with inter-cluster and intra-cluster distance among the radish genotypes

Cluster Means of Different Characters: The mean values of 18 characters for five clusters are summarized in Table 3 and fig 3. Maximum seed germination (%) was recorded in cluster II (82.00), followed by cluster IV (81.04), cluster V (79.19), cluster I (79.12), and cluster III (78.65). Maximum plant height (cm) was recorded in cluster IV (57.59), followed by cluster V (54.43), cluster I (53.80), cluster III (53.07), and cluster II (52.00). The maximum number of leaves per plant was recorded in cluster IV (14.67), followed by cluster V (14.40), cluster III (13.33), cluster II (12.00), and cluster I (11.67). Maximum leaf length (cm) was recorded in cluster IV (31.14), followed by cluster I (30.35), cluster III (29.44), cluster V (29.21), and cluster II (27.19). Maximum leaf width (cm) was recorded in cluster I (9.99), followed by cluster IV (9.88), cluster II (8.88), cluster III (8.51), and cluster V (8.09). Maximum days taken to maturity were recorded in cluster V (56.49), followed by cluster I (53.30), cluster II (52.92), cluster III (49.98), and cluster IV (49.96). Maximum average plant weight (g) was recorded in cluster IV (310.06), followed by cluster I (298.95), cluster III (289.55), cluster V (255.97), and cluster II (232.63). Maximum average root weight and crown diameter (mm) were observed for cluster IV (215.76 and 19.41), followed by cluster V (204.68 and 18.99), cluster III (203.17 and 18.89), cluster I (184.77 and 17.74), and cluster II (147.27 and 16.68), respectively. Maximum root length (23.09) was recorded in cluster IV, followed by cluster V (21.34), cluster III (20.37), cluster II (20.32), and cluster I (19.40). Maximum root diameter (mm) was recorded in cluster II (34.39), followed by cluster IV (33.96), cluster III (32.04), cluster I (31.77), and cluster V (31.38). Maximum root yield per plot (Kg) was recorded in cluster IV (5.41), followed by cluster III (4.86), cluster I (4.78), cluster II (4.30), and cluster V (4.28). Maximum root-shoot ratio (weight basis) was recorded in cluster IV (3.08), followed by cluster V (2.16), cluster I (2.01), cluster II (1.99), and cluster III (1.56). Maximum root shoot ratio (length basis) was recorded in cluster IV (0.86), followed by cluster I (0.76), cluster III (0.67), cluster V (0.55), and cluster II (0.49). Maximum total soluble solid (°B) was recorded in cluster II (5.30), followed by cluster V (5.20), cluster IV (5.03), cluster III (5.00), and cluster I (4.29). Maximum ascorbic acid (mg/100g) was recorded in cluster V (23.33), followed by cluster I (22.29), cluster III (22.00), cluster IV (17.73), and cluster II (15.23). Maximum dry matter (%) was recorded in cluster I (6.00), followed by cluster II (5.10), cluster IV (5.02), cluster III (4.53), and cluster V (4.14). and the maximum root yield ha-1 was observed for cluster V (239.01), followed by cluster IV (234.27), cluster II (225.94), cluster III (192.33), and cluster I (165.89). The results showed that there were high variations in mean values among the five clusters for all characters. Therefore, the genotypes with high mean values according to that purpose should be selected.

The above comparison indicated that cluster IV had the highest mean value for the following characters: plant height (cm), number of leaves per plant, leaf length (cm), average plant weight (gm), average root weight (gm), crown diameter (mm), root length (cm), root yield per plot (Kg), root shoot ratio based on weight, and root shoot ratio based on length. Cluster V had exhibited superior characteristics for days taken to maturity, ascorbic acid (mg/100 g), and root yield per hectare (q). Cluster II had a high mean value for seed germination (%), root diameter (mm), root yield per plot (Kg) and total soluble solid (°B) and cluster I for leaf width (cm) and dry matter (%). However, cluster III had the lowest mean values for almost all important characters. The crossing between the genotypes, which show high mean values coupled with relatively large inter-cluster D^2 values, results in high heterotic expression [16].

In the present study, genotypes from cluster IV and V indicated the highest mean values for various desirable characters and a relatively high inter-cluster D^2 value; therefore, these two genotypes can be selected for hybridization to develop a high root yielding variety of radish. The results of this study could also be helpful in improving knowledge of the divergences among the evaluated radish genotypes and would be basic to select appropriate methods in radish improvement programs and other utilizations. Earlier workers have also indicated the significance of genetic divergence in radish for different traits [10,17,18,19,20,].

Table 3: Clusters means of different characters in radish

S.N.	Characters	Cluster Mean				
		I	II	III	IV	V
1	Seed germination (%)	79.12	82.00	78.65	81.04	79.19
2	Plant height (cm)	53.80	52.00	53.07	57.59	54.43
3	Number of leaves per plant	11.67	12.00	13.33	14.67	14.40
4	Leaf length (cm)	30.35	27.19	29.44	31.14	29.21
5	Leaf width (cm)	9.99	8.88	8.51	9.88	8.09
6	Days taken to maturity	53.30	52.92	49.98	49.96	56.49
7	Average plant weight (gm)	298.95	232.63	289.55	310.06	255.97
8	Average root weight (gm)	184.77	147.27	203.17	215.76	204.68
9	Crown diameter (mm)	17.74	16.68	18.89	19.41	18.99
10	Root length (cm)	19.40	20.32	20.37	23.09	21.34
11	Root diameter (mm)	31.77	34.39	32.04	33.96	31.38
12	Root yield per plot (Kg)	4.78	4.30	4.86	5.41	4.28
13	Root shoot ratio (Weight basis)	2.01	1.99	1.56	3.08	2.16
14	Root shoot ratio (Length basis)	0.76	0.49	0.67	0.86	0.55

15	Total soluble solid (ºB)	4.29	5.30	5.00	5.03	5.20
16	Ascorbic acid (mg/100gm)	22.29	15.23	22.00	17.73	23.33
17	Dry matter (%)	6.00	5.10	4.53	5.02	4.14
18	Root yield per ha (q)	165.89	225.94	192.33	234.27	239.01

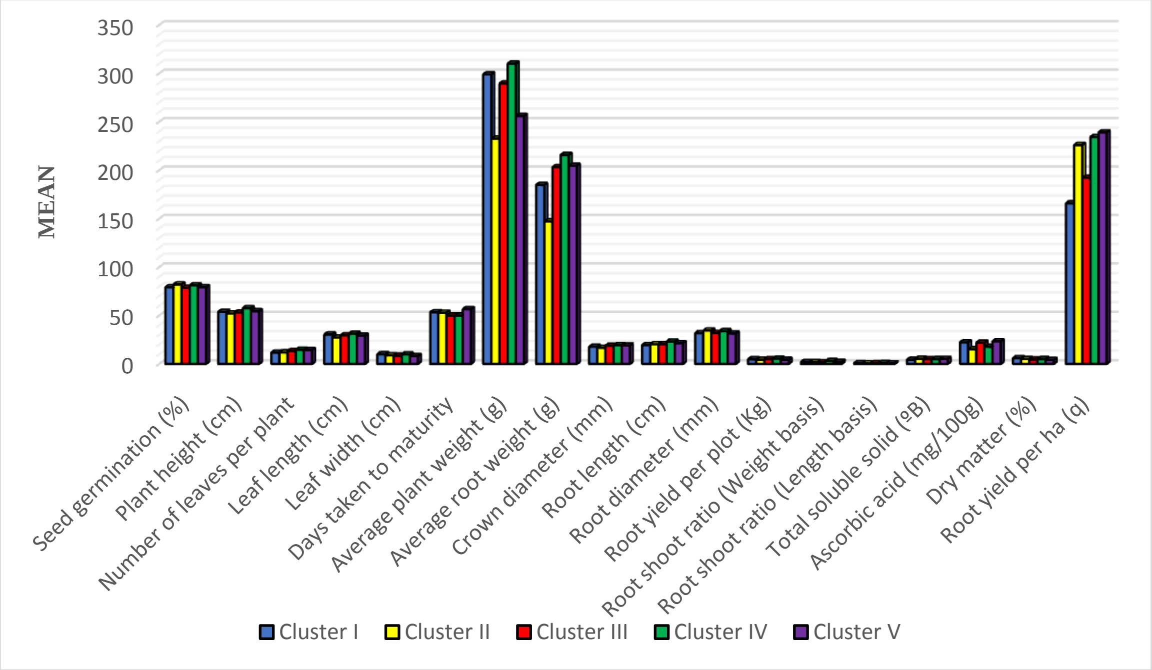

Fig 3: Clusters means of different characters in radish

Conclusion

It was concluded from the present study that there is a great deal of variation present in the genotypes, which provides a potential base for improvement as well as hybrid development in future breeding programs. Genotypes to be used as parents in future hybridization programs should be selected from diverse clusters showing maximum inter-cluster distance, and these parents (genotypes) should have high performance for the traits contributing most to divergence. Crossing genotypes with a high mean and high inter-cluster distance may also result in greater heterotic expression and a broad spectrum of favourable genetic variability in segregating generations for improvement in the root yield of radish.

Authors' contributions: 'Author A' designed the study, performed the statistical analysis, wrote the protocol, managed the literature searches, wrote the first draft of the manuscript, and managed the analyses of the study. All authors read and approved the final manuscript.

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